

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of

DAVIS, Peter D.

Atty. Ref.: **620-179**

Serial No. **10/018,826**

Group:

Filed: **December 21, 2001**

Examiner:

For: **CHIMERIC PROTEINS MEDIATING TARGETED
APOPTOSIS**

* * * * *

April 22, 2002

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

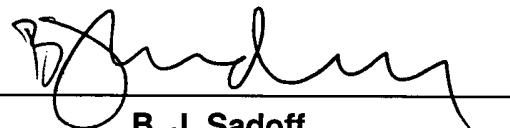
STATEMENT

The attached paper and computer-readable copies of the Sequence Listing are the same. No new matter has been added.

Respectfully submitted,

NIXON & VANDERHYE P.C.

By: _____



B. J. Sadoff

Reg. No. **36,663**

BJS:eaw

1100 North Glebe Road, 8th Floor
Arlington, VA 22201-4714
Telephone: (703) 816-4000
Facsimile: (703) 816-4100

SEQUENCE LISTING

<110> Davis, Peter D

<120> Chimeric proteins mediating targeted apoptosis

<130> 620-179

<140> US 10/018,826

<141> 2001-12-21

<150> PCT/GB00/02449

<151> 2000-06-26

<150> GB 9914650.8

<151> 1999-06-24

<160> 22

<170> PatentIn Ver. 2.1

<210> 1

<211> 84

<212> PRT

<213> Homo sapiens

<400> 1

Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys
1 5 10 15

Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile
20 25 30

Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu
35 40 45

Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu
50 55 60

Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Glu Lys Ile
65 70 75 80

Gln Thr Ile Ile

<210> 2

<211> 86

<212> PRT

<213> Homo sapiens

<400> 2

Pro Ala Thr Leu Tyr Ala Val Val Glu Asn Val Pro Pro Leu Arg Trp
1 5 10 15

```
<210> 3
<211> 1468
<212> DNA
<213> Artificial Sequence
```

```
<220>
<221> CDS
<222> (116)..(1411)
```

<220>
<223> Description of Artificial Sequence: Nucleic acid construct encoding a chimeric protein containing the extracellular domain of CD44H and the transmembrane and cytoplasmic domains of human Fas

<400> 3																60	
ccagcctctg	ccaggttcgg	tccgccatcc	tcgtcccgtc	ctccgccggc	ccctgccccg												
cgcccaggga	tcctccagct	cctttcgccc	gcgccctccg	ttcgctccgg	acacc	atg										118	
						Met											
						1											
gac	aag	ttt	tgg	tgg	cac	gca	gcc	tgg	gga	ctc	tgc	ctc	gtg	ccg	ctg		166
Asp	Lys	Phe	Trp	Trp	His	Ala	Ala	Trp	Gly	Leu	Cys	Leu	Val	Pro	Leu		
			5				10				15						
agc	ctg	gcg	cag	atc	gat	ttg	aat	ata	acc	tgc	cgc	ttt	gca	ggg	gta		214
Ser	Leu	Ala	Gln	Ile	Asp	Leu	Asn	Ile	Thr	Cys	Arg	Phe	Ala	Gly	Val		
			20				25				30						
ttc	cac	gtg	gag	aaa	aat	ggg	cgc	tac	agc	atc	tct	cgg	acg	gag	gcc		262
Phe	His	Val	Glu	Lys	Asn	Gly	Arg	Tyr	Ser	Ile	Ser	Arg	Thr	Glu	Ala		
			35				40				45						
gct	gac	ctc	tgc	aag	gct	ttc	aat	agc	acc	ttg	ccc	aca	atg	gcc	cag		310
Ala	Asp	Leu	Cys	Lys	Ala	Phe	Asn	Ser	Thr	Leu	Pro	Thr	Met	Ala	Gln		
			50				55				60				65		
atg	gag	aaa	gct	ctg	agc	atc	gga	ttt	gag	acc	tgc	agg	tat	ggg	ttc		358
Met	Glu	Lys	Ala	Leu	Ser	Ile	Gly	Phe	Glu	Thr	Cys	Arg	Tyr	Gly	Phe		
			70				75				80						

ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt	406
Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys	
85 90 95	
gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag	454
Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln	
100 105 110	
tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt	502
Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys	
115 120 125	
aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata	550
Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile	
130 135 140 145	
act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac	598
Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr	
150 155 160	
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac	646
Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp	
165 170 175	
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac	694
Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr	
180 185 190	
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt	742
Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser	
195 200 205	
ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa	790
Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln	
210 215 220 225	
gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gga tct gaa	838
Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu	
230 235 240	
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc	886
Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr	
245 250 255	
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ctt	934
Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu	
260 265 270	
tgt ctt ctt ctt ttg cca att cca cta att gtt tgg gtg aag aga aag	982
Cys Leu Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys	
275 280 285	
gaa gta cag aaa aca tgc aga aag cac aga aag gaa aac caa ggt tct	1030
Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser	
290 295 300 305	

```

cat gaa tct cca acc tta aat cct gaa aca gtg gca ata aat tta tct 1078
His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu Ser
          310                      315                      320

gat gtt gac ttg agt aaa tat atc acc act att gct gga gtc atg aca 1126
Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr
          325                      330                      335

cta agt caa gtt aaa ggc ttt gtt cga aag aat ggt gtc aat gaa gcc 1174
Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala
          340                      345                      350

aaa ata gat gag atc aag aat gac aat gtc caa gac aca gca gaa cag 1222
Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln
          355                      360                      365

aaa gtt caa ctg ctt cgt aat tgg cat caa ctt cat gga aag aaa gaa 1270
Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu
          370                      375                      380                      385

gcg tat gac aca ttg att aaa gat ctc aaa aaa gcc aat ctt tgt act 1318
Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr
          390                      395                      400

ctt gca ggg aaa att cag act atc atc ctc aag gac att act agt gac 1366
Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp
          405                      410                      415

tca gaa aat tca aac ttc aga aat gaa atc caa agc ttg gtc tag 1411
Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
          420                      425                      430

agtgaaaaaac aacaaattca gttctgagta tatgcaatta gtgtttgaaa agattct 1468

```

<210> 4

<211> 431

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chimeric protein
containing the extracellular domain of CD44H and the
transmembrane and cytoplasmic domains of human Fas

<400> 4

```

Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
 1          5          10          15
Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
          20          25          30
Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
          35          40          45
Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
          50          55          60
Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
          65          70          75          80

```

Phe	Ile	Glu	Gly	His	Val	Val	Ile	Pro	Arg	Ile	His	Pro	Asn	Ser	Ile	85	90	95
Cys	Ala	Ala	Asn	Asn	Thr	Gly	Val	Tyr	Ile	Leu	Thr	Tyr	Asn	Thr	Ser	100	105	110
Gln	Tyr	Asp	Thr	Tyr	Cys	Phe	Asn	Ala	Ser	Ala	Pro	Pro	Glu	Glu	Asp	115	120	125
Cys	Thr	Ser	Val	Thr	Asp	Leu	Pro	Asn	Ala	Phe	Asp	Gly	Pro	Ile	Thr	130	135	140
Ile	Thr	Ile	Val	Asn	Arg	Asp	Gly	Thr	Arg	Tyr	Val	Gln	Lys	Gly	Glu	145	150	155
Tyr	Arg	Thr	Asn	Pro	Glu	Asp	Ile	Tyr	Pro	Ser	Asn	Pro	Thr	Asp	Asp	165	170	175
Asp	Val	Ser	Ser	Gly	Ser	Ser	Ser	Glu	Arg	Ser	Ser	Thr	Ser	Gly	Gly	180	185	190
Tyr	Ile	Phe	Tyr	Thr	Phe	Ser	Thr	Val	His	Pro	Ile	Pro	Asp	Glu	Asp	195	200	205
Ser	Pro	Trp	Ile	Thr	Asp	Ser	Thr	Asp	Arg	Ile	Pro	Ala	Thr	Arg	Asp	210	215	220
Gln	Asp	Thr	Phe	His	Pro	Ser	Gly	Gly	Ser	His	Thr	Thr	His	Gly	Ser	225	230	235
Glu	Ser	Asp	Gly	His	Ser	His	Gly	Ser	Gln	Glu	Gly	Gly	Ala	Asn	Thr	245	250	255
Thr	Ser	Gly	Pro	Ile	Arg	Thr	Pro	Gln	Ile	Pro	Glu	Trp	Leu	Ile	Ile	260	265	270
Leu	Cys	Leu	Leu	Leu	Leu	Pro	Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg	275	280	285
Lys	Glu	Val	Gln	Lys	Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly	290	295	300
Ser	His	Glu	Ser	Pro	Thr	Leu	Asn	Pro	Glu	Thr	Val	Ala	Ile	Asn	Leu	305	310	315
Ser	Asp	Val	Asp	Leu	Ser	Lys	Tyr	Ile	Thr	Thr	Ile	Ala	Gly	Val	Met	325	330	335
Thr	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg	Lys	Asn	Gly	Val	Asn	Glu	340	345	350
Ala	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp	Asn	Val	Gln	Asp	Thr	Ala	Glu	355	360	365
Gln	Lys	Val	Gln	Leu	Leu	Arg	Asn	Trp	His	Gln	Leu	His	Gly	Lys	Lys	370	375	380
Glu	Ala	Tyr	Asp	Thr	Leu	Ile	Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys	385	390	395
Thr	Leu	Ala	Gly	Lys	Ile	Gln	Thr	Ile	Ile	Leu	Lys	Asp	Ile	Thr	Ser	405	410	415
Asp	Ser	Glu	Asn	Ser	Asn	Phe	Arg	Asn	Glu	Ile	Gln	Ser	Leu	Val		420	425	430

<210> 5
 <211> 1483
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (116)..(1426)

<220>
 <223> Description of Artificial Sequence: Nucleic acid
 construct encoding a chimeric protein containing
 the extracellular and transmembrane domains of CD44H
 and the cytoplasmic domain of human Fas

<400> 5
 ccagcctctg ccagggttcgg tccgccatcc tcgtcccgtc ctccgccggc ccctgccccg 60
 cgcccaggga tcctccagct cctttcgccc gcgccttcg ttcgctccgg acacc atg 118
 Met
 1
 gac aag ttt tgg tgg cac gca gcc tgg gga ctc tgc ctc gtg ccg ctg 166
 Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro Leu
 5 10 15
 agc ctg gcg cag atc gat ttg aat ata acc tgc cgc ttt gca ggt gta 214
 Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly Val
 20 25 30
 ttc cac gtg gag aaa aat ggt cgc tac agc atc tct cgg acg gag gcc 262
 Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu Ala
 35 40 45
 gct gac ctc tgc aag gct ttc aat agc acc ttg ccc aca atg gcc cag 310
 Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala Gln
 50 55 60 65
 atg gag aaa gct ctg agc atc gga ttt gag acc tgc agg tat ggg ttc 358
 Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly Phe
 70 75 80
 ata gaa ggg cat gtg gtg att ccc cgg atc cac ccc aac tcc atc tgt 406
 Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile Cys
 85 90 95
 gca gca aac aac aca ggg gtg tac atc ctc aca tac aac acc tcc cag 454
 Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser Gln
 100 105 110
 tat gac aca tat tgc ttc aat gct tca gct cca cct gaa gaa gat tgt 502
 Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp Cys
 115 120 125
 aca tca gtc aca gac ctg ccc aat gcc ttt gat gga cca att acc ata 550
 Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr Ile
 130 135 140 145

act att gtt aac cgt gat ggc acc cgc tat gtc cag aaa gga gaa tac	598
Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu Tyr	
150 155 160	
aga acg aat cct gaa gac atc tac ccc agc aac cct act gat gat gac	646
Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp Asp	
165 170 175	
gtg agc agc ggc tcc tcc agt gaa agg agc agc act tca gga ggt tac	694
Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly Tyr	
180 185 190	
atc ttt tac acc ttt tct act gta cac ccc atc cca gac gaa gac agt	742
Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp Ser	
195 200 205	
ccc tgg atc acc gac agc aca gac aga atc cct gct acc aga gac caa	790
Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp Gln	
210 215 220 225	
gac aca ttc cac ccc agt ggg ggg tcc cat acc act cat gga tct gaa	838
Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser Glu	
230 235 240	
tca gat gga cac tca cat ggg agt caa gaa ggt gga gca aac aca acc	886
Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr Thr	
245 250 255	
tct ggt cct ata agg aca ccc caa att cca gaa tgg ctg atc atc ttg	934
Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile Leu	
260 265 270	
gca tcc ctc ttg gcc ttg gct ttg att ctt gca gtt tgc att gca gtc	982
Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala Val	
275 280 285	
ggg gtg aag aga aag gaa gta cag aaa aca tgc aga aag cac aga aag	1030
Gly Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg Lys	
290 295 300 305	
gaa aac caa ggt tct cat gaa tct cca acc tta aat cct gaa aca gtg	1078
Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr Val	
310 315 320	
gca ata aat tta tct gat gtt gac ttg agt aaa tat atc acc act att	1126
Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr Ile	
325 330 335	
gct gga gtc atg aca cta agt caa gtt aaa ggc ttt gtt cga aag aat	1174
Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys Asn	
340 345 350	
ggt gtc aat gaa gcc aaa ata gat gag atc aag aat gac aat gtc caa	1222
Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val Gln	
355 360 365	

gac aca gca gaa cag aaa gtt caa ctg ctt cgt aat tgg cat caa ctt 1270
 Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln Leu
 370 375 380 385

 cat gga aag aaa gaa gcg tat gac aca ttg att aaa gat ctc aaa aaa 1318
 His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys Lys
 390 395 400

 gcc aat ctt tgt act ctt gca ggg aaa att cag act atc atc ctc aag 1366
 Ala Asn Leu Cys Thr Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu Lys
 405 410 415

 gac att act agt gac tca gaa aat tca aac ttc aga aat gaa atc caa 1414
 Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile Gln
 420 425 430

 agc ttg gtc tag agtgaaaaac aacaaattca gttctgagta tatgcaatta 1466
 Ser Leu Val
 435

 gtgttttgaag agattct 1483

<210> 6
 <211> 436
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Chimeric protein
 containing the extracellular and transmembrane domains
 of CD44H and the cytoplasmic domain of human Fas

<400> 6
 Met Asp Lys Phe Trp Trp His Ala Ala Trp Gly Leu Cys Leu Val Pro
 1 5 10 15
 Leu Ser Leu Ala Gln Ile Asp Leu Asn Ile Thr Cys Arg Phe Ala Gly
 20 25 30
 Val Phe His Val Glu Lys Asn Gly Arg Tyr Ser Ile Ser Arg Thr Glu
 35 40 45
 Ala Ala Asp Leu Cys Lys Ala Phe Asn Ser Thr Leu Pro Thr Met Ala
 50 55 60
 Gln Met Glu Lys Ala Leu Ser Ile Gly Phe Glu Thr Cys Arg Tyr Gly
 65 70 75 80
 Phe Ile Glu Gly His Val Val Ile Pro Arg Ile His Pro Asn Ser Ile
 85 90 95
 Cys Ala Ala Asn Asn Thr Gly Val Tyr Ile Leu Thr Tyr Asn Thr Ser
 100 105 110
 Gln Tyr Asp Thr Tyr Cys Phe Asn Ala Ser Ala Pro Pro Glu Glu Asp
 115 120 125
 Cys Thr Ser Val Thr Asp Leu Pro Asn Ala Phe Asp Gly Pro Ile Thr
 130 135 140
 Ile Thr Ile Val Asn Arg Asp Gly Thr Arg Tyr Val Gln Lys Gly Glu
 145 150 155 160
 Tyr Arg Thr Asn Pro Glu Asp Ile Tyr Pro Ser Asn Pro Thr Asp Asp
 165 170 175

Asp Val Ser Ser Gly Ser Ser Ser Glu Arg Ser Ser Thr Ser Gly Gly
 180 185 190
 Tyr Ile Phe Tyr Thr Phe Ser Thr Val His Pro Ile Pro Asp Glu Asp
 195 200 205
 Ser Pro Trp Ile Thr Asp Ser Thr Asp Arg Ile Pro Ala Thr Arg Asp
 210 215 220
 Gln Asp Thr Phe His Pro Ser Gly Gly Ser His Thr Thr His Gly Ser
 225 230 235 240
 Glu Ser Asp Gly His Ser His Gly Ser Gln Glu Gly Gly Ala Asn Thr
 245 250 255
 Thr Ser Gly Pro Ile Arg Thr Pro Gln Ile Pro Glu Trp Leu Ile Ile
 260 265 270
 Leu Ala Ser Leu Leu Ala Leu Ala Leu Ile Leu Ala Val Cys Ile Ala
 275 280 285
 Val Gly Val Lys Arg Lys Glu Val Gln Lys Thr Cys Arg Lys His Arg
 290 295 300
 Lys Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu Asn Pro Glu Thr
 305 310 315 320
 Val Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys Tyr Ile Thr Thr
 325 330 335
 Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly Phe Val Arg Lys
 340 345 350
 Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys Asn Asp Asn Val
 355 360 365
 Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg Asn Trp His Gln
 370 375 380
 Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile Lys Asp Leu Lys
 385 390 395 400
 Lys Ala Asn Leu Cys Thr Leu Ala Gly Lys Ile Gln Thr Ile Ile Leu
 405 410 415
 Lys Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe Arg Asn Glu Ile
 420 425 430
 Gln Ser Leu Val
 435

<210> 7

<211> 3009

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (190)..(2952)

<220>

<223> Description of Artificial Sequence: Nucleic acid construct
 encoding chimeric protein containing the extracellular
 domain of Flt-1 fused in-frame to the transmembrane and
 cytoplasmic domains of Fas

<400> 7

gcgggtaccg cggccagcgg gcctggcggc gaggattacc cggggaagtg gttgtctcct 60

ggctggagcc gcgagacggg cgctcagggc gcggggccgg cggcggcgaa cgagaggacg 120

gactctggcg gccgggtcgt tggccggggg agcgcgggca ccgggagc aggccgcgtc 180

gcgctcacc atg gtc agc tac tgg gac acc ggg gtc ctg ctg tgc gcg ctg 231
Met Val Ser Tyr Trp Asp Thr Gly Val Leu Leu Cys Ala Leu

1

5

10

ctc agc tgt ctg ctt ctc aca gga tct agt tca ggt tca aaa tta aaa 279
Leu Ser Cys Leu Leu Leu Thr Gly Ser Ser Ser Gly Ser Lys Leu Lys
15 20 25 30

gat cct gaa ctg agt tta aaa ggc acc cag cac atc atg caa gca ggc 327
Asp Pro Glu Leu Ser Leu Lys Gly Thr Gln His Ile Met Gln Ala Gly
35 40 45

cag aca ctg cat ctc caa tgc agg ggg gaa gca gcc cat aaa tgg tct 375
Gln Thr Leu His Leu Gln Cys Arg Gly Glu Ala Ala His Lys Trp Ser
50 55 60

ttg cct gaa atg gtg agt aag gaa agc gaa agg ctg agc ata act aaa 423
Leu Pro Glu Met Val Ser Lys Glu Ser Glu Arg Leu Ser Ile Thr Lys
65 70 75

tct gcc tgt gga aga aat ggc aaa caa ttc tgc agt act tta acc ttg 471
Ser Ala Cys Gly Arg Asn Gly Lys Gln Phe Cys Ser Thr Leu Thr Leu
80 85 90

aac aca gct caa gca aac cac act ggc ttc tac agc tgc aaa tat cta 519
Asn Thr Ala Gln Ala Asn His Thr Gly Phe Tyr Ser Cys Lys Tyr Leu
95 100 105 110

gct gta cct act tca aag aag aag gaa aca gaa tct gca atc tat ata 567
Ala Val Pro Thr Ser Lys Lys Lys Glu Thr Glu Ser Ala Ile Tyr Ile
115 120 125

ttt att agt gat aca ggt aga cct ttc gta gag atg tac agt gaa atc 615
Phe Ile Ser Asp Thr Gly Arg Pro Phe Val Glu Met Tyr Ser Glu Ile
130 135 140

ccc gaa att ata cac atg act gaa gga agg gag ctc gtc att ccc tgc 663
Pro Glu Ile Ile His Met Thr Glu Gly Arg Glu Leu Val Ile Pro Cys
145 150 155

cgg gtt acg tca cct aac atc act gtt act tta aaa aag ttt cca ctt 711
Arg Val Thr Ser Pro Asn Ile Thr Val Thr Leu Lys Lys Phe Pro Leu
160 165 170

gac act ttg atc cct gat gga aaa cgc ata atc tgg gac agt aga aag 759
Asp Thr Leu Ile Pro Asp Gly Lys Arg Ile Ile Trp Asp Ser Arg Lys
175 180 185 190

ggc ttc atc ata tca aat gca acg tac aaa gaa ata ggg ctt ctg acc 807
Gly Phe Ile Ile Ser Asn Ala Thr Tyr Lys Glu Ile Gly Leu Leu Thr
195 200 205

tgt gaa gca aca gtc aat ggg cat ttg tat aag aca aac tat ctc aca 855
Cys Glu Ala Thr Val Asn Gly His Leu Tyr Lys Thr Asn Tyr Leu Thr
210 215 220

cat	cga	caa	acc	aat	aca	atc	ata	gat	gtc	caa	ata	agc	aca	cca	cgc	903
His	Arg	Gln	Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	
		225					230					235				
cca	gtc	aaa	tta	ctt	aga	ggc	cat	act	ctt	gtc	ctc	aat	tgt	act	gct	951
Pro	Val	Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	
	240					245					250					
acc	act	ccc	ttg	aac	acg	aga	gtt	caa	atg	acc	tgg	agt	tac	cct	gat	999
Thr	Thr	Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	
255					260					265					270	
gaa	aaa	aat	aag	aga	gct	tcc	gta	agg	cga	cga	att	gac	caa	agc	aat	1047
Glu	Lys	Asn	Lys	Arg	Ala	Ser	Val	Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	
				275					280					285		
tcc	cat	gcc	aac	ata	ttc	tac	agt	gtt	ctt	act	att	gac	aaa	atg	cag	1095
Ser	His	Ala	Asn	Ile	Phe	Tyr	Ser	Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	
			290					295					300			
aac	aaa	gac	aaa	gga	ctt	tat	act	tgt	cgt	gta	agg	agt	gga	cca	tca	1143
Asn	Lys	Asp	Lys	Gly	Leu	Tyr	Thr	Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	
		305					310					315				
ttc	aaa	tct	gtt	aac	acc	tca	gtg	cat	ata	tat	gat	aaa	gca	ttc	atc	1191
Phe	Lys	Ser	Val	Asn	Thr	Ser	Val	His	Ile	Tyr	Asp	Lys	Ala	Phe	Ile	
	320					325					330					
act	gtg	aaa	cat	cga	aaa	cag	cag	gtg	ctt	gaa	acc	gta	gct	ggc	aag	1239
Thr	Val	Lys	His	Arg	Lys	Gln	Gln	Val	Leu	Glu	Thr	Val	Ala	Gly	Lys	
335					340					345					350	
cgg	tct	tac	cgg	ctc	tct	atg	aaa	gtg	aag	gca	ttt	ccc	tcg	ccg	gaa	1287
Arg	Ser	Tyr	Arg	Leu	Ser	Met	Lys	Val	Lys	Ala	Phe	Pro	Ser	Pro	Glu	
				355					360					365		
gtt	gta	tgg	tta	aaa	gat	ggg	tta	cct	gcg	act	gag	aaa	tct	gct	cgc	1335
Val	Val	Trp	Leu	Lys	Asp	Gly	Leu	Pro	Ala	Thr	Glu	Lys	Ser	Ala	Arg	
			370					375					380			
tat	ttg	act	cgt	ggc	tac	tcg	tta	att	atc	aag	gac	gta	act	gaa	gag	1383
Tyr	Leu	Thr	Arg	Gly	Tyr	Ser	Leu	Ile	Ile	Lys	Asp	Val	Thr	Glu	Glu	
		385					390					395				
gat	gca	ggg	aat	tat	aca	atc	ttg	ctg	agc	ata	aaa	cag	tca	aat	gtg	1431
Asp	Ala	Gly	Asn	Tyr	Thr	Ile	Leu	Leu	Ser	Ile	Lys	Gln	Ser	Asn	Val	
	400					405					410					
ttt	aaa	aac	ctc	act	gcc	act	cta	att	gtc	aat	gtg	aaa	ccc	cag	att	1479
Phe	Lys	Asn	Leu	Thr	Ala	Thr	Leu	Ile	Val	Asn	Val	Lys	Pro	Gln	Ile	
415					420					425					430	
tac	gaa	aag	gcc	gtg	tca	tcg	ttt	cca	gac	ccg	gct	ctc	tac	cca	ctg	1527
Tyr	Glu	Lys	Ala	Val	Ser	Ser	Phe	Pro	Asp	Pro	Ala	Leu	Tyr	Pro	Leu	
				435					440					445		

ggc agc aga caa atc ctg act tgt acc gca tat ggt atc cct caa cct	1575
Gly Ser Arg Gln Ile Leu Thr Cys Thr Ala Tyr Gly Ile Pro Gln Pro	
450 455 460	
aca atc aag tgg ttc tgg cac ccc tgt aac cat aat cat tcc gaa gca	1623
Thr Ile Lys Trp Phe Trp His Pro Cys Asn His Asn His Ser Glu Ala	
465 470 475	
agg tgt gac ttt tgt tcc aat aat gaa gag tcc ttt atc ctg gat gct	1671
Arg Cys Asp Phe Cys Ser Asn Asn Glu Glu Ser Phe Ile Leu Asp Ala	
480 485 490	
gac agc aac atg gga aac aga att gag agc atc act cag cgc atg gca	1719
Asp Ser Asn Met Gly Asn Arg Ile Glu Ser Ile Thr Gln Arg Met Ala	
495 500 505 510	
ata ata gaa gga aag aat aag atg gct agc acc ttg gtt gtg gct gac	1767
Ile Ile Glu Gly Lys Asn Lys Met Ala Ser Thr Leu Val Val Ala Asp	
515 520 525	
tct aga att tct gga atc tac att tgc ata gct tcc aat aaa gtt ggg	1815
Ser Arg Ile Ser Gly Ile Tyr Ile Cys Ile Ala Ser Asn Lys Val Gly	
530 535 540	
act gtg gga aga aac ata agc ttt tat atc aca gat gtg cca aat ggg	1863
Thr Val Gly Arg Asn Ile Ser Phe Tyr Ile Thr Asp Val Pro Asn Gly	
545 550 555	
ttt cat gtt aac ttg gaa aaa atg ccg acg gaa gga gag gac ctg aaa	1911
Phe His Val Asn Leu Glu Lys Met Pro Thr Glu Gly Glu Asp Leu Lys	
560 565 570	
ctg tct tgc aca gtt aac aag ttc tta tac aga gac gtt act tgg att	1959
Leu Ser Cys Thr Val Asn Lys Phe Leu Tyr Arg Asp Val Thr Trp Ile	
575 580 585 590	
tta ctg cgg aca gtt aat aac aga aca atg cac tac agt att agc aag	2007
Leu Leu Arg Thr Val Asn Asn Arg Thr Met His Tyr Ser Ile Ser Lys	
595 600 605	
caa aaa atg gcc atc act aag gag cac tcc atc act ctt aat ctt acc	2055
Gln Lys Met Ala Ile Thr Lys Glu His Ser Ile Thr Leu Asn Leu Thr	
610 615 620	
atc atg aat gtt tcc ctg caa gat tca ggc acc tat gcc tgc aga gcc	2103
Ile Met Asn Val Ser Leu Gln Asp Ser Gly Thr Tyr Ala Cys Arg Ala	
625 630 635	
agg aat gta tac aca ggg gaa gaa atc ctc cag aag aaa gaa att aca	2151
Arg Asn Val Tyr Thr Gly Glu Glu Ile Leu Gln Lys Lys Glu Ile Thr	
640 645 650	
atc aga gat cag gaa gca cca tac ctc ctg cga aac ctc agt gat cac	2199
Ile Arg Asp Gln Glu Ala Pro Tyr Leu Leu Arg Asn Leu Ser Asp His	
655 660 665 670	

aca	gtg	gcc	atc	agc	agt	tcc	acc	act	tta	gac	tgt	cat	gct	aat	ggg	2247
Thr	Val	Ala	Ile	Ser	Ser	Ser	Thr	Thr	Leu	Asp	Cys	His	Ala	Asn	Gly	
				675					680						685	
gtc	ccc	gag	cct	cag	atc	act	tgg	ttt	aaa	aac	aac	cac	aaa	ata	caa	2295
Val	Pro	Glu	Pro	Gln	Ile	Thr	Trp	Phe	Lys	Asn	Asn	His	Lys	Ile	Gln	
			690					695					700			
caa	gag	cct	gga	att	att	tta	gga	cca	gga	agc	agc	acg	ctg	ttt	att	2343
Gln	Glu	Pro	Gly	Ile	Ile	Leu	Gly	Pro	Gly	Ser	Ser	Thr	Leu	Phe	Ile	
		705					710					715				
gaa	aga	gtc	aca	gaa	gag	gat	gaa	ggg	gtc	tat	cac	tgc	aaa	gcc	acc	2391
Glu	Arg	Val	Thr	Glu	Glu	Asp	Glu	Gly	Val	Tyr	His	Cys	Lys	Ala	Thr	
	720					725					730					
aac	cag	aag	ggc	tct	gtg	gaa	agt	tca	gca	tac	ctc	act	gtt	caa	gga	2439
Asn	Gln	Lys	Gly	Ser	Val	Glu	Ser	Ser	Ala	Tyr	Leu	Thr	Val	Gln	Gly	
	735				740					745					750	
acc	tcg	gac	gga	tcc	aga	tct	aac	ttg	ggg	tgg	ctt	tgt	ctt	ctt	ctt	2487
Thr	Ser	Asp	Gly	Ser	Arg	Ser	Asn	Leu	Gly	Trp	Leu	Cys	Leu	Leu	Leu	
			755						760					765		
ttg	cca	att	cca	cta	att	gtt	tgg	gtg	aag	aga	aag	gaa	gta	cag	aaa	2535
Leu	Pro	Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg	Lys	Glu	Val	Gln	Lys	
			770					775					780			
aca	tgc	aga	aag	cac	aga	aag	gaa	aac	caa	ggg	tct	cat	gaa	tct	cca	2583
Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly	Ser	His	Glu	Ser	Pro	
		785					790					795				
acc	tta	aat	cct	gaa	aca	gtg	gca	ata	aat	tta	tct	gat	gtt	gac	ttg	2631
Thr	Leu	Asn	Pro	Glu	Thr	Val	Ala	Ile	Asn	Leu	Ser	Asp	Val	Asp	Leu	
	800					805					810					
agt	aaa	tat	atc	acc	act	att	gct	gga	gtc	atg	aca	cta	agt	caa	gtt	2679
Ser	Lys	Tyr	Ile	Thr	Thr	Ile	Ala	Gly	Val	Met	Thr	Leu	Ser	Gln	Val	
	815				820					825					830	
aaa	ggc	ttt	gtt	cga	aag	aat	ggg	gtc	aat	gaa	gcc	aaa	ata	gat	gag	2727
Lys	Gly	Phe	Val	Arg	Lys	Asn	Gly	Val	Asn	Glu	Ala	Lys	Ile	Asp	Glu	
			835					840						845		
atc	aag	aat	gac	aat	gtc	caa	gac	aca	gca	gaa	cag	aaa	gtt	caa	ctg	2775
Ile	Lys	Asn	Asp	Asn	Val	Gln	Asp	Thr	Ala	Glu	Gln	Lys	Val	Gln	Leu	
			850					855					860			
ctt	cgt	aat	tgg	cat	caa	ctt	cat	gga	aag	aaa	gaa	gcg	tat	gac	aca	2823
Leu	Arg	Asn	Trp	His	Gln	Leu	His	Gly	Lys	Lys	Glu	Ala	Tyr	Asp	Thr	
		865					870					875				
ttg	att	aaa	gat	ctc	aaa	aaa	gcc	aat	ctt	tgt	act	ctt	gca	ggg	aaa	2871
Leu	Ile	Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys	Thr	Leu	Ala	Gly	Lys	
	880					885					890					

att cag act atc atc ctc aag gac att act agt gac tca gaa aat tca 2919
 Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser Glu Asn Ser
 895 900 905 910

aac ttc aga aat gaa atc caa agc ttg gtc tag agtgaaaaac aacaaattca 2972
 Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
 915 920

gttctgagta tatgcaatta gtgtttgaaa agattct 3009

<210> 8

<211> 920

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chimeric protein
 containing the extracellular domain of Flt-1 fused
 in-frame to the transmembrane and cytoplasmic domains
 of Fas

<400> 8

Met	Val	Ser	Tyr	Trp	Asp	Thr	Gly	Val	Leu	Leu	Cys	Ala	Leu	Leu	Ser	1	5	10	15
Cys	Leu	Leu	Leu	Thr	Gly	Ser	Ser	Ser	Gly	Ser	Lys	Leu	Lys	Asp	Pro	20	25	30	
Glu	Leu	Ser	Leu	Lys	Gly	Thr	Gln	His	Ile	Met	Gln	Ala	Gly	Gln	Thr	35	40	45	
Leu	His	Leu	Gln	Cys	Arg	Gly	Glu	Ala	Ala	His	Lys	Trp	Ser	Leu	Pro	50	55	60	
Glu	Met	Val	Ser	Lys	Glu	Ser	Glu	Arg	Leu	Ser	Ile	Thr	Lys	Ser	Ala	65	70	75	80
Cys	Gly	Arg	Asn	Gly	Lys	Gln	Phe	Cys	Ser	Thr	Leu	Thr	Leu	Asn	Thr	85	90	95	
Ala	Gln	Ala	Asn	His	Thr	Gly	Phe	Tyr	Ser	Cys	Lys	Tyr	Leu	Ala	Val	100	105	110	
Pro	Thr	Ser	Lys	Lys	Lys	Glu	Thr	Glu	Ser	Ala	Ile	Tyr	Ile	Phe	Ile	115	120	125	
Ser	Asp	Thr	Gly	Arg	Pro	Phe	Val	Glu	Met	Tyr	Ser	Glu	Ile	Pro	Glu	130	135	140	
Ile	Ile	His	Met	Thr	Glu	Gly	Arg	Glu	Leu	Val	Ile	Pro	Cys	Arg	Val	145	150	155	160
Thr	Ser	Pro	Asn	Ile	Thr	Val	Thr	Leu	Lys	Lys	Phe	Pro	Leu	Asp	Thr	165	170	175	
Leu	Ile	Pro	Asp	Gly	Lys	Arg	Ile	Ile	Trp	Asp	Ser	Arg	Lys	Gly	Phe	180	185	190	
Ile	Ile	Ser	Asn	Ala	Thr	Tyr	Lys	Glu	Ile	Gly	Leu	Leu	Thr	Cys	Glu	195	200	205	
Ala	Thr	Val	Asn	Gly	His	Leu	Tyr	Lys	Thr	Asn	Tyr	Leu	Thr	His	Arg	210	215	220	
Gln	Thr	Asn	Thr	Ile	Ile	Asp	Val	Gln	Ile	Ser	Thr	Pro	Arg	Pro	Val	225	230	235	240
Lys	Leu	Leu	Arg	Gly	His	Thr	Leu	Val	Leu	Asn	Cys	Thr	Ala	Thr	Thr	245	250	255	
Pro	Leu	Asn	Thr	Arg	Val	Gln	Met	Thr	Trp	Ser	Tyr	Pro	Asp	Glu	Lys	260	265	270	

Asn	Lys	Arg	Ala	Ser	Val	Arg	Arg	Arg	Ile	Asp	Gln	Ser	Asn	Ser	His
		275						280				285			
Ala	Asn	Ile	Phe	Tyr	Ser	Val	Leu	Thr	Ile	Asp	Lys	Met	Gln	Asn	Lys
	290					295					300				
Asp	Lys	Gly	Leu	Tyr	Thr	Cys	Arg	Val	Arg	Ser	Gly	Pro	Ser	Phe	Lys
305					310					315					320
Ser	Val	Asn	Thr	Ser	Val	His	Ile	Tyr	Asp	Lys	Ala	Phe	Ile	Thr	Val
				325					330					335	
Lys	His	Arg	Lys	Gln	Gln	Val	Leu	Glu	Thr	Val	Ala	Gly	Lys	Arg	Ser
			340					345					350		
Tyr	Arg	Leu	Ser	Met	Lys	Val	Lys	Ala	Phe	Pro	Ser	Pro	Glu	Val	Val
	355						360					365			
Trp	Leu	Lys	Asp	Gly	Leu	Pro	Ala	Thr	Glu	Lys	Ser	Ala	Arg	Tyr	Leu
	370					375					380				
Thr	Arg	Gly	Tyr	Ser	Leu	Ile	Ile	Lys	Asp	Val	Thr	Glu	Glu	Asp	Ala
385					390					395					400
Gly	Asn	Tyr	Thr	Ile	Leu	Leu	Ser	Ile	Lys	Gln	Ser	Asn	Val	Phe	Lys
				405					410					415	
Asn	Leu	Thr	Ala	Thr	Leu	Ile	Val	Asn	Val	Lys	Pro	Gln	Ile	Tyr	Glu
			420					425					430		
Lys	Ala	Val	Ser	Ser	Phe	Pro	Asp	Pro	Ala	Leu	Tyr	Pro	Leu	Gly	Ser
	435						440					445			
Arg	Gln	Ile	Leu	Thr	Cys	Thr	Ala	Tyr	Gly	Ile	Pro	Gln	Pro	Thr	Ile
	450					455					460				
Lys	Trp	Phe	Trp	His	Pro	Cys	Asn	His	Asn	His	Ser	Glu	Ala	Arg	Cys
465					470					475					480
Asp	Phe	Cys	Ser	Asn	Asn	Glu	Glu	Ser	Phe	Ile	Leu	Asp	Ala	Asp	Ser
				485					490					495	
Asn	Met	Gly	Asn	Arg	Ile	Glu	Ser	Ile	Thr	Gln	Arg	Met	Ala	Ile	Ile
			500					505					510		
Glu	Gly	Lys	Asn	Lys	Met	Ala	Ser	Thr	Leu	Val	Val	Ala	Asp	Ser	Arg
	515						520					525			
Ile	Ser	Gly	Ile	Tyr	Ile	Cys	Ile	Ala	Ser	Asn	Lys	Val	Gly	Thr	Val
	530					535					540				
Gly	Arg	Asn	Ile	Ser	Phe	Tyr	Ile	Thr	Asp	Val	Pro	Asn	Gly	Phe	His
545					550					555					560
Val	Asn	Leu	Glu	Lys	Met	Pro	Thr	Glu	Gly	Glu	Asp	Leu	Lys	Leu	Ser
				565					570					575	
Cys	Thr	Val	Asn	Lys	Phe	Leu	Tyr	Arg	Asp	Val	Thr	Trp	Ile	Leu	Leu
			580					585					590		
Arg	Thr	Val	Asn	Asn	Arg	Thr	Met	His	Tyr	Ser	Ile	Ser	Lys	Gln	Lys
	595						600					605			
Met	Ala	Ile	Thr	Lys	Glu	His	Ser	Ile	Thr	Leu	Asn	Leu	Thr	Ile	Met
	610					615					620				
Asn	Val	Ser	Leu	Gln	Asp	Ser	Gly	Thr	Tyr	Ala	Cys	Arg	Ala	Arg	Asn
625					630					635					640
Val	Tyr	Thr	Gly	Glu	Glu	Ile	Leu	Gln	Lys	Lys	Glu	Ile	Thr	Ile	Arg
				645					650					655	
Asp	Gln	Glu	Ala	Pro	Tyr	Leu	Leu	Arg	Asn	Leu	Ser	Asp	His	Thr	Val
			660					665				670			
Ala	Ile	Ser	Ser	Ser	Thr	Thr	Leu	Asp	Cys	His	Ala	Asn	Gly	Val	Pro
	675						680					685			
Glu	Pro	Gln	Ile	Thr	Trp	Phe	Lys	Asn	Asn	His	Lys	Ile	Gln	Gln	Glu
	690					695					700				
Pro	Gly	Ile	Ile	Leu	Gly	Pro	Gly	Ser	Ser	Thr	Leu	Phe	Ile	Glu	Arg
705					710					715					720


```

Val Thr Glu Glu Asp Glu Gly Val Tyr His Cys Lys Ala Thr Asn Gln
      725                      730                      735
Lys Gly Ser Val Glu Ser Ser Ala Tyr Leu Thr Val Gln Gly Thr Ser
      740                      745                      750
Asp Gly Ser Arg Ser Asn Leu Gly Trp Leu Cys Leu Leu Leu Leu Pro
      755                      760                      765
Ile Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val Gln Lys Thr Cys
      770                      775                      780
Arg Lys His Arg Lys Glu Asn Gln Gly Ser His Glu Ser Pro Thr Leu
      785                      790                      795
Asn Pro Glu Thr Val Ala Ile Asn Leu Ser Asp Val Asp Leu Ser Lys
      805                      810                      815
Tyr Ile Thr Thr Ile Ala Gly Val Met Thr Leu Ser Gln Val Lys Gly
      820                      825                      830
Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile Asp Glu Ile Lys
      835                      840                      845
Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val Gln Leu Leu Arg
      850                      855                      860
Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr Asp Thr Leu Ile
      865                      870                      875
Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala Gly Lys Ile Gln
      885                      890                      895
Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser Glu Asn Ser Asn Phe
      900                      905                      910
Arg Asn Glu Ile Gln Ser Leu Val
      915                      920

```

```

<210> 9
<211> 3009
<212> DNA
<213> Artificial Sequence

```

```

<220>
<221> CDS
<222> (169)..(2952)

```

```

<220>
<223> Description of Artificial Sequence: Nucleic acid construct
      encoding chimeric protein containing the extracellular
      domain of Flk-1 fused in-frame to the transmembrane and
      cytoplasmic domains of Fas

```

```

<400> 9
gcgggtaccg ccgcccgtcg gcgcccgggc tccctagccc tgtgcgctca actgtcctgc 60
gctgcgggggt gccgcgagtt ccacctccgc gcctccttct ctagacaggc gctgggagaa 120
agaaccggct cccgagttct gggcatttcg cccggctcga ggtgcagg atg cag agc 177
                                     Met Gln Ser
                                     1

aag gtg ctg ctg gcc gtc gcc ctg tgg ctc tgc gtg gag acc cgg gcc 225
Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu Thr Arg Ala
      5                      10                      15

```

gcc tct gtg ggt ttg cct agt gtt tct ctt gat ctg ccc agg ctc agc	273
Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro Arg Leu Ser	
20 25 30 35	
ata caa aaa gac ata ctt aca att aag gct aat aca act ctt caa att	321
Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr Leu Gln Ile	
40 45 50	
act tgc agg gga cag agg gac ttg gac tgg ctt tgg ccc aat aat cag	369
Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro Asn Asn Gln	
55 60 65	
agt ggc agt gag caa agg gtg gag gtg act gag tgc agc gat ggc ctc	417
Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser Asp Gly Leu	
70 75 80	
ttc tgt aag aca ctc aca att cca aaa gtg atc gga aat gac act gga	465
Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn Asp Thr Gly	
85 90 95	
gcc tac aag tgc ttc tac cgg gaa act gac ttg gcc tcg gtc att tat	513
Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser Val Ile Tyr	
100 105 110 115	
gtc tat gtt caa gat tac aga tct cca ttt att gct tct gtt agt gac	561
Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser Val Ser Asp	
120 125 130	
caa cat gga gtc gtg tac att act gag aac aaa aac aaa act gtg gtg	609
Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys Thr Val Val	
135 140 145	
att cca tgt ctc ggg tcc att tca aat ctc aac gtg tca ctt tgt gca	657
Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser Leu Cys Ala	
150 155 160	
aga tac cca gaa aag aga ttt gtt cct gat ggt aac aga att tcc tgg	705
Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg Ile Ser Trp	
165 170 175	
gac agc aag aag ggc ttt act att ccc agc tac atg atc agc tat gct	753
Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile Ser Tyr Ala	
180 185 190 195	
ggc atg gtc ttc tgt gaa gca aaa att aat gat gaa agt tac cag tct	801
Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser Tyr Gln Ser	
200 205 210	
att atg tac ata gtt gtc gtt gta ggg tat agg att tat gat gtg gtt	849
Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr Asp Val Val	
215 220 225	
ctg agt ccg tct cat gga att gaa cta tct gtt gga gaa aag ctt gtc	897
Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu Lys Leu Val	
230 235 240	

tta aat tgt aca gca aga act gaa cta aat gtg ggg att gac ttc aac	945
Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile Asp Phe Asn	
245 250 255	
tgg gaa tac cct tct tcg aag cat cag cat aag aaa ctt gta aac cga	993
Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu Val Asn Arg	
260 265 270 275	
gac cta aaa acc cag tct ggg agt gag atg aag aaa ttt ttg agc acc	1041
Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe Leu Ser Thr	
280 285 290	
tta act ata gat ggt gta acc cgg agt gac caa gga ttg tac acc tgt	1089
Leu Thr Ile Asp Gly Val Thr Arg Ser Asp Gln Gly Leu Tyr Thr Cys	
295 300 305	
gca gca tcc agt ggg ctg atg acc aag aag aac agc aca ttt gtc agg	1137
Ala Ala Ser Ser Gly Leu Met Thr Lys Lys Asn Ser Thr Phe Val Arg	
310 315 320	
gtc cat gaa aaa cct ttt gtt gct ttt gga agt ggc atg gaa tct ctg	1185
Val His Glu Lys Pro Phe Val Ala Phe Gly Ser Gly Met Glu Ser Leu	
325 330 335	
gtg gaa gcc acg gtg ggg gag cgt gtc aga atc cct gcg aag tac ctt	1233
Val Glu Ala Thr Val Gly Glu Arg Val Arg Ile Pro Ala Lys Tyr Leu	
340 345 350 355	
ggt tac cca ccc cca gaa ata aaa tgg tat aaa aat gga ata ccc ctt	1281
Gly Tyr Pro Pro Pro Glu Ile Lys Trp Tyr Lys Asn Gly Ile Pro Leu	
360 365 370	
gag tcc aat cac aca att aaa gcg ggg cat gta ctg acg att atg gaa	1329
Glu Ser Asn His Thr Ile Lys Ala Gly His Val Leu Thr Ile Met Glu	
375 380 385	
gtg agt gaa aga gac aca gga aat tac act gtc atc ctt acc aat ccc	1377
Val Ser Glu Arg Asp Thr Gly Asn Tyr Thr Val Ile Leu Thr Asn Pro	
390 395 400	
att tca aag gag aag cag agc cat gtg gtc tct ctg gtt gtg tat gtc	1425
Ile Ser Lys Glu Lys Gln Ser His Val Val Ser Leu Val Val Tyr Val	
405 410 415	
cca ccc cag att ggt gag aaa tct cta atc tct cct gtg gat tcc tac	1473
Pro Pro Gln Ile Gly Glu Lys Ser Leu Ile Ser Pro Val Asp Ser Tyr	
420 425 430 435	
cag tac ggc acc act caa acg ctg aca tgt acg gtc tat gcc att cct	1521
Gln Tyr Gly Thr Thr Gln Thr Leu Thr Cys Thr Val Tyr Ala Ile Pro	
440 445 450	
ccc ccg cat cac atc cac tgg tat tgg cag ttg gag gaa gag tgc gcc	1569
Pro Pro His His Ile His Trp Tyr Trp Gln Leu Glu Glu Glu Cys Ala	
455 460 465	

aac gag ccc agc caa gct gtc tca gtg aca aac cca tac cct tgt gaa	1617
Asn Glu Pro Ser Gln Ala Val Ser Val Thr Asn Pro Tyr Pro Cys Glu	
470 475 480	
gaa tgg aga agt gtg gag gac ttc cag gga gga aat aaa att gaa gtt	1665
Glu Trp Arg Ser Val Glu Asp Phe Gln Gly Gly Asn Lys Ile Glu Val	
485 490 495	
aat aaa aat caa ttt gct cta att gaa gga aaa aac aaa act gta agt	1713
Asn Lys Asn Gln Phe Ala Leu Ile Glu Gly Lys Asn Lys Thr Val Ser	
500 505 510 515	
acc ctt gtt atc caa gcg gca aat gtg tca gct ttg tac aaa tgt gaa	1761
Thr Leu Val Ile Gln Ala Ala Asn Val Ser Ala Leu Tyr Lys Cys Glu	
520 525 530	
gcg gtc aac aaa gtc ggg aga gga gag agg gtg atc tcc ttc cac gtg	1809
Ala Val Asn Lys Val Gly Arg Gly Glu Arg Val Ile Ser Phe His Val	
535 540 545	
acc agg ggt cct gaa att act ttg caa cct gac atg cag ccc act gag	1857
Thr Arg Gly Pro Glu Ile Thr Leu Gln Pro Asp Met Gln Pro Thr Glu	
550 555 560	
cag gag agc gtg tct ttg tgg tgc act gca gac aga tct acg ttt gag	1905
Gln Glu Ser Val Ser Leu Trp Cys Thr Ala Asp Arg Ser Thr Phe Glu	
565 570 575	
aac ctc aca tgg tac aag ctt ggc cca cag cct ctg cca atc cat gtg	1953
Asn Leu Thr Trp Tyr Lys Leu Gly Pro Gln Pro Leu Pro Ile His Val	
580 585 590 595	
gga gag ttg ccc aca cct gtt tgc aag aac ttg gat act ctt tgg aaa	2001
Gly Glu Leu Pro Thr Pro Val Cys Lys Asn Leu Asp Thr Leu Trp Lys	
600 605 610	
ttg aat gcc acc atg ttc tct aat agc aca aat gac att ttg atc atg	2049
Leu Asn Ala Thr Met Phe Ser Asn Ser Thr Asn Asp Ile Leu Ile Met	
615 620 625	
gag ctt aag aat gca tcc ttg cag gac caa gga gac tat gtc tgc ctt	2097
Glu Leu Lys Asn Ala Ser Leu Gln Asp Gln Gly Asp Tyr Val Cys Leu	
630 635 640	
gct caa gac agg aag acc aag aaa aga cat tgc gtg gtc agg cag ctc	2145
Ala Gln Asp Arg Lys Thr Lys Lys Arg His Cys Val Val Arg Gln Leu	
645 650 655	
aca gtc cta gag cgt gtg gca ccc acg atc aca gga aac ctg gag aat	2193
Thr Val Leu Glu Arg Val Ala Pro Thr Ile Thr Gly Asn Leu Glu Asn	
660 665 670 675	
cag acg aca agt att ggg gaa agc atc gaa gtc tca tgc acg gca tct	2241
Gln Thr Thr Ser Ile Gly Glu Ser Ile Glu Val Ser Cys Thr Ala Ser	
680 685 690	

ggg aat ccc cct cca cag atc atg tgg ttt aaa gat aat gag acc ctt	2289
Gly Asn Pro Pro Pro Gln Ile Met Trp Phe Lys Asp Asn Glu Thr Leu	
695 700 705	
gta gaa gac tca ggc att gta ttg aag gat ggg aac cgg aac ctc act	2337
Val Glu Asp Ser Gly Ile Val Leu Lys Asp Gly Asn Arg Asn Leu Thr	
710 715 720	
atc cgc aga gtg agg aag gag gac gaa ggc ctc tac acc tgc cag gca	2385
Ile Arg Arg Val Arg Lys Glu Asp Glu Gly Leu Tyr Thr Cys Gln Ala	
725 730 735	
tgc agt gtt ctt ggc tgt gca aaa gtg gag gca ttt ttc ata ata gaa	2433
Cys Ser Val Leu Gly Cys Ala Lys Val Glu Ala Phe Phe Ile Ile Glu	
740 745 750 755	
ggg gcc cag gaa aag gga tcc aga tct aac ttg ggg tgg ctt tgt ctt	2481
Gly Ala Gln Glu Lys Gly Ser Arg Ser Asn Leu Gly Trp Leu Cys Leu	
760 765 770	
ctt ctt ttg cca att cca cta att gtt tgg gtg aag aga aag gaa gta	2529
Leu Leu Leu Pro Ile Pro Leu Ile Val Trp Val Lys Arg Lys Glu Val	
775 780 785	
cag aaa aca tgc aga aag cac aga aag gaa aac caa ggt tct cat gaa	2577
Gln Lys Thr Cys Arg Lys His Arg Lys Glu Asn Gln Gly Ser His Glu	
790 795 800	
tct cca acc tta aat cct gaa aca gtg gca ata aat tta tct gat gtt	2625
Ser Pro Thr Leu Asn Pro Glu Thr Val Ala Ile Asn Leu Ser Asp Val	
805 810 815	
gac ttg agt aaa tat atc acc act att gct gga gtc atg aca cta agt	2673
Asp Leu Ser Lys Tyr Ile Thr Thr Ile Ala Gly Val Met Thr Leu Ser	
820 825 830 835	
caa gtt aaa ggc ttt gtt cga aag aat ggt gtc aat gaa gcc aaa ata	2721
Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile	
840 845 850	
gat gag atc aag aat gac aat gtc caa gac aca gca gaa cag aaa gtt	2769
Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val	
855 860 865	
caa ctg ctt cgt aat tgg cat caa ctt cat gga aag aaa gaa gcg tat	2817
Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr	
870 875 880	
gac aca ttg att aaa gat ctc aaa aaa gcc aat ctt tgt act ctt gca	2865
Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala	
885 890 895	
ggg aaa att cag act atc atc ctc aag gac att act agt gac tca gaa	2913
Gly Lys Ile Gln Thr Ile Ile Leu Lys Asp Ile Thr Ser Asp Ser Glu	
900 905 910 915	

aat tca aac ttc aga aat gaa atc caa agc ttg gtc tag agtgaaaaac 2962
 Asn Ser Asn Phe Arg Asn Glu Ile Gln Ser Leu Val
 920 925

aacaaattca gttctgagta tatgcaatta gtgtttgaaa agattct 3009

<210> 10

<211> 927

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Chimeric protein
 containing the extracellular domain of Flk-1 fused
 in-frame to the transmembrane and cytoplasmic domains
 of Fas

<400> 10

Met Gln Ser Lys Val Leu Leu Ala Val Ala Leu Trp Leu Cys Val Glu
 1 5 10 15
 Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro
 20 25 30
 Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr
 35 40 45
 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro
 50 55 60
 Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser
 65 70 75 80
 Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn
 85 90 95
 Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser
 100 105 110
 Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser
 115 120 125
 Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys
 130 135 140
 Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser
 145 150 155 160
 Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg
 165 170 175
 Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile
 180 185 190
 Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser
 195 200 205
 Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr
 210 215 220
 Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu
 225 230 235 240
 Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile
 245 250 255
 Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu
 260 265 270
 Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe
 275 280 285

Leu	Ser	Thr	Leu	Thr	Ile	Asp	Gly	Val	Thr	Arg	Ser	Asp	Gln	Gly	Leu
290						295					300				
Tyr	Thr	Cys	Ala	Ala	Ser	Ser	Gly	Leu	Met	Thr	Lys	Lys	Asn	Ser	Thr
305					310					315					320
Phe	Val	Arg	Val	His	Glu	Lys	Pro	Phe	Val	Ala	Phe	Gly	Ser	Gly	Met
				325					330					335	
Glu	Ser	Leu	Val	Glu	Ala	Thr	Val	Gly	Glu	Arg	Val	Arg	Ile	Pro	Ala
			340					345					350		
Lys	Tyr	Leu	Gly	Tyr	Pro	Pro	Pro	Glu	Ile	Lys	Trp	Tyr	Lys	Asn	Gly
		355					360					365			
Ile	Pro	Leu	Glu	Ser	Asn	His	Thr	Ile	Lys	Ala	Gly	His	Val	Leu	Thr
	370					375					380				
Ile	Met	Glu	Val	Ser	Glu	Arg	Asp	Thr	Gly	Asn	Tyr	Thr	Val	Ile	Leu
385					390					395					400
Thr	Asn	Pro	Ile	Ser	Lys	Glu	Lys	Gln	Ser	His	Val	Val	Ser	Leu	Val
				405					410					415	
Val	Tyr	Val	Pro	Pro	Gln	Ile	Gly	Glu	Lys	Ser	Leu	Ile	Ser	Pro	Val
			420					425					430		
Asp	Ser	Tyr	Gln	Tyr	Gly	Thr	Thr	Gln	Thr	Leu	Thr	Cys	Thr	Val	Tyr
		435					440					445			
Ala	Ile	Pro	Pro	Pro	His	His	Ile	His	Trp	Tyr	Trp	Gln	Leu	Glu	Glu
	450					455						460			
Glu	Cys	Ala	Asn	Glu	Pro	Ser	Gln	Ala	Val	Ser	Val	Thr	Asn	Pro	Tyr
465					470					475					480
Pro	Cys	Glu	Glu	Trp	Arg	Ser	Val	Glu	Asp	Phe	Gln	Gly	Gly	Asn	Lys
				485					490					495	
Ile	Glu	Val	Asn	Lys	Asn	Gln	Phe	Ala	Leu	Ile	Glu	Gly	Lys	Asn	Lys
		500						505					510		
Thr	Val	Ser	Thr	Leu	Val	Ile	Gln	Ala	Ala	Asn	Val	Ser	Ala	Leu	Tyr
		515					520					525			
Lys	Cys	Glu	Ala	Val	Asn	Lys	Val	Gly	Arg	Gly	Glu	Arg	Val	Ile	Ser
	530					535					540				
Phe	His	Val	Thr	Arg	Gly	Pro	Glu	Ile	Thr	Leu	Gln	Pro	Asp	Met	Gln
545					550					555					560
Pro	Thr	Glu	Gln	Glu	Ser	Val	Ser	Leu	Trp	Cys	Thr	Ala	Asp	Arg	Ser
				565					570					575	
Thr	Phe	Glu	Asn	Leu	Thr	Trp	Tyr	Lys	Leu	Gly	Pro	Gln	Pro	Leu	Pro
			580					585					590		
Ile	His	Val	Gly	Glu	Leu	Pro	Thr	Pro	Val	Cys	Lys	Asn	Leu	Asp	Thr
	595					600						605			
Leu	Trp	Lys	Leu	Asn	Ala	Thr	Met	Phe	Ser	Asn	Ser	Thr	Asn	Asp	Ile
	610					615					620				
Leu	Ile	Met	Glu	Leu	Lys	Asn	Ala	Ser	Leu	Gln	Asp	Gln	Gly	Asp	Tyr
625					630					635					640
Val	Cys	Leu	Ala	Gln	Asp	Arg	Lys	Thr	Lys	Lys	Arg	His	Cys	Val	Val
				645					650					655	
Arg	Gln	Leu	Thr	Val	Leu	Glu	Arg	Val	Ala	Pro	Thr	Ile	Thr	Gly	Asn
			660					665					670		
Leu	Glu	Asn	Gln	Thr	Thr	Ser	Ile	Gly	Glu	Ser	Ile	Glu	Val	Ser	Cys
		675				680						685			
Thr	Ala	Ser	Gly	Asn	Pro	Pro	Pro	Gln	Ile	Met	Trp	Phe	Lys	Asp	Asn
	690				695					700					
Glu	Thr	Leu	Val	Glu	Asp	Ser	Gly	Ile	Val	Leu	Lys	Asp	Gly	Asn	Arg
705					710					715					720
Asn	Leu	Thr	Ile	Arg	Arg	Val	Arg	Lys	Glu	Asp	Glu	Gly	Leu	Tyr	Thr
				725					730					735	

Cys	Gln	Ala	Cys	Ser	Val	Leu	Gly	Cys	Ala	Lys	Val	Glu	Ala	Phe	Phe		
			740					745					750				
Ile	Ile	Glu	Gly	Ala	Gln	Glu	Lys	Gly	Ser	Arg	Ser	Asn	Leu	Gly	Trp		
		755					760					765					
Leu	Cys	Leu	Leu	Leu	Leu	Pro	Ile	Pro	Leu	Ile	Val	Trp	Val	Lys	Arg		
	770					775					780						
Lys	Glu	Val	Gln	Lys	Thr	Cys	Arg	Lys	His	Arg	Lys	Glu	Asn	Gln	Gly		
785					790					795					800		
Ser	His	Glu	Ser	Pro	Thr	Leu	Asn	Pro	Glu	Thr	Val	Ala	Ile	Asn	Leu		
				805					810					815			
Ser	Asp	Val	Asp	Leu	Ser	Lys	Tyr	Ile	Thr	Thr	Ile	Ala	Gly	Val	Met		
		820						825					830				
Thr	Leu	Ser	Gln	Val	Lys	Gly	Phe	Val	Arg	Lys	Asn	Gly	Val	Asn	Glu		
		835					840					845					
Ala	Lys	Ile	Asp	Glu	Ile	Lys	Asn	Asp	Asn	Val	Gln	Asp	Thr	Ala	Glu		
	850					855					860						
Gln	Lys	Val	Gln	Leu	Leu	Arg	Asn	Trp	His	Gln	Leu	His	Gly	Lys	Lys		
865					870					875					880		
Glu	Ala	Tyr	Asp	Thr	Leu	Ile	Lys	Asp	Leu	Lys	Lys	Ala	Asn	Leu	Cys		
			885					890						895			
Thr	Leu	Ala	Gly	Lys	Ile	Gln	Thr	Ile	Ile	Leu	Lys	Asp	Ile	Thr	Ser		
		900						905					910				
Asp	Ser	Glu	Asn	Ser	Asn	Phe	Arg	Asn	Glu	Ile	Gln	Ser	Leu	Val			
		915					920					925					

<210> 11

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 11

gcggaattca ggggcgggca ctggcac

27

<210> 12

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 12

ggctcgagaa tcttttcaaa cactaattgc

30

<210> 13

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 13

aacgtgatca tcctttgtct tcttcttttg

30

<210> 14

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 14

gcccggggtg aagagaaagg aagtacag

28

<210> 15

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

gcgggtaccg cggccagcgg gcctggcgcc

30

<210> 16

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

ggcggatccg tccgagggtc cttgaacagt gagg

34

<210> 17

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 17

gcgggtaccg ccgcccgtcg gcgcccgggc

30

<400> 22

gatggagttg aaggtagttt cgtg

24



Creation date: 31-07-2003
Indexing Officer: VPHAN - VU PHAN
Team: OIPEBackFileIndexing
Dossier: 10018826

Legal Date: 21-05-2002

No.	Doccode	Number of pages
1	CRFL	6

Total number of pages: 6

Remarks:

Order of re-scan issued on